RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/561,040_
Source: _IFWP_
Date Processed by STIC: _12/6/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 12/06/2006
PATENT APPLICATION: **US/10/561,040**   TIME: 10:10:57

Input Set : **A:\P28994.APP**
Output Set: **N:\CRF4\12062006\J561040.raw**

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 3 <110> APPLICANT: MIYAWAKI, ATSUSHI
 4        TSUTSUI, HIDEKAZU
 5        KARASAWA, SATOSHI
 7 <120> TITLE OF INVENTION: FLUORESCENT PROTEIN
 9 <130> FILE REFERENCE: P28994
11 <140> CURRENT APPLICATION NUMBER: 10/561,040
12 <141> CURRENT FILING DATE: 2005-12-16
14 <150> PRIOR APPLICATION NUMBER: PCT/JP04/08790
15 <151> PRIOR FILING DATE: 2004-06-16
17 <150> PRIOR APPLICATION NUMBER: JP 2003-170330
18 <151> PRIOR FILING DATE: 2003-06-16
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 227
26 <212> TYPE: PRT
27 <213> ORGANISM: Favia favus
29 <400> SEQUENCE: 1
30 Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Leu Met Glu Gly
31  1               5                   10                  15
33 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
34                 20                  25                  30
36 Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
37             35                  40                  45
39 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe Asp Tyr Gly
40         50                  55                  60
42 Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
43  65                  70                  75                  80
45 Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
46                 85                  90                  95
48 Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
49                 100                 105                 110
51 Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
52             115                 120                 125
54 Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
55         130                 135                 140
57 Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
58 145                 150                 155                 160
60 Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
61                 165                 170                 175
63 Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
64             180                 185                 190
66 Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
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67   195   200   205
69 Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
70   210   215   220
72 Leu Ala Lys
73 225
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 684
78 <212> TYPE: DNA
79 <213> ORGANISM: Favia favus
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)..(681)
85 <400> SEQUENCE: 2
86 atg agt gtg att aca tca gaa atg aag atg gag ctg ctt atg gaa ggc   48
87 Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Leu Met Glu Gly
88 1   5   10   15
90 gct gta aac ggg cac aag ttc gtg att aca ggg aaa gga agt ggc cag   96
91 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
92   20   25   30
94 cct ttc gag gga ata cag aat atg gac ctg aca gtc ata gag ggc gga   144
95 Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
96   35   40   45
98 cct ctt cct ttt gct ttc gat atc ctg aca aca gta ttc gat tac ggc   192
99 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe Asp Tyr Gly
100   50   55   60
102 aac cgg gta ttt gtc aaa tac cca gaa gaa ata gta gac tac ttc aag   240
103 Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
104 65   70   75   80
106 cag tcg ttt cct gag ggt tat tct tgg gaa cga agc atg agt tac gaa   288
107 Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
108   85   90   95
110 gac ggg gga att tgc ctc gcc aca aac aat ata acg atg aag aaa gac   336
111 Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
112   100   105   110
114 ggc agc aac tgt ttt gtc tat gaa att cga ttt gat ggt gtg aac ttt   384
115 Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
116   115   120   125
118 cct gcc aat ggt cca gtt atg cag agg aag acc gtc aaa tgg gag cca   432
119 Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
120   130   135   140
122 tcc act gag aaa atg tat gtg cgt gat gga gtg ctg aag ggt gat gtt   480
123 Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
124 145   150   155   160
126 aac atg gct ctg ttg ctt caa gga ggt ggc cat tac cga tgt gac ttc   528
127 Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
128   165   170   175
130 aga act act tac aaa gca aag aag gtt gtc cag ttg cca gac tat cac   576
131 Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
132   180   185   190

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134 ttc gtg gat cat cga att gag ata aca agc cat gac aag gat tac aac    624
135 Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
136         195                 200                 205
138 aag gtt aag ctg tat gag cat gct aaa gct cat tcc ggg ctg cca agg    672
139 Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
140     210                 215                 220
142 ctg gcc aag taa                                                     684
143 Leu Ala Lys
144 225
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 23
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
154       primer
156 <220> FEATURE:
157 <221> NAME/KEY: modified_base
158 <222> LOCATION: (3)
159 <223> OTHER INFORMATION: Inosine
161 <220> FEATURE:
162 <221> NAME/KEY: modified_base
163 <222> LOCATION: (9)
164 <223> OTHER INFORMATION: Inosine
166 <220> FEATURE:
167 <221> NAME/KEY: modified_base
168 <222> LOCATION: (21)
169 <223> OTHER INFORMATION: a, c, g, t, unknown or other
171 <400> SEQUENCE: 3
W--> 172 ggnwsbgtna ayggvcayda ntt                                      23
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 27
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
182       primer
184 <400> SEQUENCE: 4
185 aactggaaga attcgcggcc gcaggaa                                       27
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 23
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
195       primer
197 <220> FEATURE:
198 <221> NAME/KEY: modified_base
199 <222> LOCATION: (11)
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             Input Set : A:\P28994.APP
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      200 <223> OTHER INFORMATION: Inosine
      202 <220> FEATURE:
      203 <221> NAME/KEY: modified_base
      204 <222> LOCATION: (14)
      205 <223> OTHER INFORMATION: Inosine
      207 <220> FEATURE:
      208 <221> NAME/KEY: modified_base
      209 <222> LOCATION: (20)
      210 <223> OTHER INFORMATION: Inosine
      212 <400> SEQUENCE: 5
W-->  213 tgccwtttgc nttngayatn ttg                            23
      216 <210> SEQ ID NO: 6
      217 <211> LENGTH: 35
      218 <212> TYPE: DNA
      219 <213> ORGANISM: Artificial Sequence
      221 <220> FEATURE:
      222 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      223       primer
      225 <220> FEATURE:
      226 <221> NAME/KEY: modified_base
      227 <222> LOCATION: (4)
      228 <223> OTHER INFORMATION: Inosine
      230 <220> FEATURE:
      231 <221> NAME/KEY: modified_base
      232 <222> LOCATION: (15)
      233 <223> OTHER INFORMATION: Inosine
      235 <220> FEATURE:
      236 <221> NAME/KEY: modified_base
      237 <222> LOCATION: (18)
      238 <223> OTHER INFORMATION: Inosine
      240 <220> FEATURE:
      241 <221> NAME/KEY: modified_base
      242 <222> LOCATION: (21)
      243 <223> OTHER INFORMATION: Inosine
      245 <400> SEQUENCE: 6
W-->  246 gtcntcttyt gcacnacngg nccatydgva ggaaa                35
      249 <210> SEQ ID NO: 7
      250 <211> LENGTH: 36
      251 <212> TYPE: DNA
      252 <213> ORGANISM: Artificial Sequence
      254 <220> FEATURE:
      255 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      256       primer
      258 <220> FEATURE:
      259 <221> NAME/KEY: modified_base
      260 <222> LOCATION: (24)..(25)
      261 <223> OTHER INFORMATION: Inosine
      263 <220> FEATURE:
      264 <221> NAME/KEY: modified_base
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RAW SEQUENCE LISTING   DATE: 12/06/2006
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            Input Set : A:\P28994.APP
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    265 <222> LOCATION: (29)..(30)
    266 <223> OTHER INFORMATION: Inosine
    268 <220> FEATURE:
    269 <221> NAME/KEY: modified_base
    270 <222> LOCATION: (34)..(35)
    271 <223> OTHER INFORMATION: Inosine
    273 <400> SEQUENCE: 7
W--> 274 ggccacgcgt cgactagtac gggnngggnn gggnng   36
    277 <210> SEQ ID NO: 8
    278 <211> LENGTH: 30
    279 <212> TYPE: DNA
    280 <213> ORGANISM: Artificial Sequence
    282 <220> FEATURE:
    283 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    284   primer
    286 <400> SEQUENCE: 8
    287 ttgtcaagat atcgaaagcg aacggcagag   30
    290 <210> SEQ ID NO: 9
    291 <211> LENGTH: 20
    292 <212> TYPE: DNA
    293 <213> ORGANISM: Artificial Sequence
    295 <220> FEATURE:
    296 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    297   primer
    299 <400> SEQUENCE: 9
    300 ggccacgcgt cgactagtac   20
    303 <210> SEQ ID NO: 10
    304 <211> LENGTH: 30
    305 <212> TYPE: DNA
    306 <213> ORGANISM: Artificial Sequence
    308 <220> FEATURE:
    309 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    310   primer
    312 <400> SEQUENCE: 10
    313 gtccaccctc tacgactttg agttccatat   30
    316 <210> SEQ ID NO: 11
    317 <211> LENGTH: 44
    318 <212> TYPE: DNA
    319 <213> ORGANISM: Artificial Sequence
    321 <220> FEATURE:
    322 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    323   primer
    325 <400> SEQUENCE: 11
    326 cccggatccg atgagtgtga ttacawcaga aatgaagatg gagc   44
    329 <210> SEQ ID NO: 12
    330 <211> LENGTH: 227
    331 <212> TYPE: PRT
    332 <213> ORGANISM: Favia favus
    334 <400> SEQUENCE: 12

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/06/2006
PATENT APPLICATION: **US/10/561,040**   TIME: 10:10:58

Input Set : **A:\P28994.APP**
Output Set: **N:\CRF4\12062006\J561040.raw**

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; N Pos. 3,9,21
Seq#:5; N Pos. 11,14,20
Seq#:6; N Pos. 4,15,18,21
Seq#:7; N Pos. 24,25,29,30,34,35

VERIFICATION SUMMARY DATE: 12/06/2006
PATENT APPLICATION: **US/10/561,040** TIME: 10:10:58

Input Set : **A:\P28994.APP**
Output Set: **N:\CRF4\12062006\J561040.raw**

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L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
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